

PT Jorgensen MU, Bang S, Olsen OH, Petersen LC;
 XX
 DR WPI; 2003-041403/03.
 XX
 PT Kunitz-type protease inhibitor used in the treatment of inflammatory
 PT disorders.
 XX
 PS Claim 20; Page 49; 52pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a 51 amino
 acid sequence being a generic sequence for a kunitz-type protease
 inhibitor or a variant where the sequence is at least 80% identical to
 the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
 included are an isolated polypeptide obtainable by cultivation of a host
 cell comprising a polynucleotide construct encoding kunitz-type protein
 in an appropriate growth medium under conditions allowing expression of
 the polynucleotide construct and recovering the polypeptide from the
 culture medium, a polynucleotide construct encoding kunitz-type protein
 and a host cell comprising the polynucleotide construct. The
 kunitz-type protein is used for the preparation of a medicament for the
 treatment of systemic inflammatory response syndrome, acute pancreatitis,
 shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
 hemorrhage, myocardial infarction, for prevention of blood loss during
 major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, embolism,
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
 CC inflammatory bowel disease, and psoriasis. The present sequence is a
 XX human HKI-18 mutant sequence
 SQ Sequence 58 AA;

Query Match 100.0%; Score 329; DB 6; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1 1e-31; Mismatches 0; Indels 0; Gaps 0;
 Matches 58; Conservative 0; MisMatch 0; Del 0; Insert 0;

Oy 1 YPVRCUPLPATGPCKARIIRWYFVASVGQCNRFVYGGCRGNANNFASEQCMSSCGS 58
 Db 1 YPVRCUPLPATGPCKARIIRWYFVASVGQCNRFVYGGCRGNANNFASEQCMSSCGS 58

RESULT 2
 ID ABG71915
 ID ABG71915 standard; protein; 58 AA.
 AC
 XX
 AC ABG71915;
 XX
 DT 22-JAN-2003 (first entry)
 XX
 DE Human Kunitz protease inhibitor protein HKI-18, mutant #2.
 XX
 KW Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
 KW anticoagulant; coagulant; cardiotant; CBP; psoriasis; emphysema;
 KW systemic inflammatory response syndrome; acute pancreatitis;
 KW shock syndrome; disseminated intravascular coagulation; mutant;
 KW hyperfibrinolytic hemorrhage; myocardial infarction; muttein;
 KW cardiopulmonary bypass-induced protease release; deep vein thrombosis;
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.

PH Key Location/Qualifiers
 PT Misc-difference 9 /note= "Wild-type Ser substituted by Pro"
 PT
 PT Misc-difference 11 /note= "Wild-type His substituted by Thr"
 PT Misc-difference 13 /note= "Wild-type Ser substituted by Pro"
 PT Misc-difference 15..19 /note= "Wild-type Ala-Asp-Trp-Ala-Ala substituted by Arg-
 PT Ala-Arg-Ile-Ile"
 PT Misc-difference 34 Misc-difference 34

Query Match 99.1%; Score 326; DB 6; Length 58;
 Best Local Similarity 98.3%; Pred. No. 2.4e-31; Mismatches 0; Indels 0; Gaps 0;
 Matches 57; Conservative 1; MisMatch 0; Del 0; Insert 0;

Oy 1 YPVRCUPLPATGPCKARIIRWYFVASVGQCNRFVYGGCRGNANNFASEQCMSSCGS 58
 Db 1 YPVRCUPLPATGPCKARIIRWYFVASVGQCNRFVYGGCRGNANNFASEQCMSSCGS 58

RESULT 3
 ID ABG71917
 ID ABG71917 standard; protein; 58 AA.
 AC
 XX
 AC ABG71917;
 XX
 DT 22-JAN-2003 (first entry)
 XX
 DE Human Kunitz protease inhibitor protein HKI-18, mutant #4.
 XX
 DE Human Kunitz protease inhibitor protein HKI-18, mutant #4.
 KW Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
 KW anticoagulant; coagulant; cardiotant; CBP; psoriasis; emphysema;
 KW systemic inflammatory response syndrome; acute pancreatitis;
 KW shock syndrome; disseminated intravascular coagulation; mutant;
 KW hyperfibrinolytic hemorrhage; myocardial infarction; muttein;
 KW cardiopulmonary bypass-induced protease release; deep vein thrombosis;
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.

XX OS Homo sapiens.
 OS Synthetic.
 XX
 FH
 FT Misc-difference 9 location/Qualifiers
 FT /note= "Wild-type Ser substituted by Pro"
 FT Misc-difference 11
 FT /note= "Wild-type His substituted by Thr"
 FT Misc-difference 13
 FT /note= "Wild-type Ser substituted by Pro"
 FT Misc-difference 15..17
 FT /note= "Wild-type Ala-Asp-Trp substituted by Lys-Ala-Arg"
 FT /note= "Wild-type Trp substituted by Val"
 XX WO200296938-A2.
 XX PD 05-DEC-2002.
 XX PF 31-MAY-2002; 2002WO-DK000372.
 XX PR 31-MAY-2001; 2001DK-00000859.
 PR 05-JUL-2001; 2001US-0303180P.
 PA (NOVO) NOVO NORDISK AS.
 XX PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;
 XX DR WPI; 2003-041403/03.
 XX PT Kunitz-type protease inhibitor used in the treatment of inflammatory
 PT disorders.
 XX PS Claim 20; Page 49; 52pp; English.
 XX CC The invention relates to an isolated polypeptide comprising a 51 amino
 acid sequence being a generic sequence for a Kunitz-type protease
 inhibitor or a variant where the sequence is at least 80% identical to
 the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
 included are an isolated polypeptide obtainable by cultivation of a host
 cell comprising a polynucleotide construct encoding kunitz-type protein
 in an appropriate growth medium under conditions allowing expression of
 the polynucleotide construct and recovering the polypeptide from the
 culture medium, a polynucleotide construct encoding the kunitz-type
 protein and a host cell comprising the polynucleotide construct. The
 kunitz-type protein is used for the preparation of a medicament for the
 treatment of systemic inflammatory response syndrome, acute pancreatitis,
 shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
 haemorrhage, myocardial infarction, for prevention of blood loss during
 major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
 allergy-induced protease release, deep vein thrombosis, emphysema,
 rheumatoid arthritis, adult respiratory distress syndrome, chronic
 inflammatory bowel disease, and psoriasis. The present sequence is a
 CC human HKI-18 mutant sequence
 XX SQ Sequence 58 AA;

Query Match 95.4%; Score 314; DB 6; Length 58;
 Best Local Similarity 94.8%; Pred. No. 6..6-30;
 Matches 55; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YPYRCLIPPATGPCKARIRTRWYFWAVSGCNRFRYGGRRGNANNFASFOECMSSCGS 58
 Db 1 YPYRCLIPPATGPCKARIRTRWYFWAVSGCNRFRYGGRRGNANNFASFOECMSSCGS 58

RESULT 4
 ABC71920
 ID ABC71920 standard; protein; 111 AA.
 AC ABC71920;
 XX

DT 22-JAN-2003 (first entry)
 XX DE Human 212L-HKI-18-2 fusion protein.
 XX KW Human; protease inhibitor; kunitz; HKI-18; antiinflammatory; mutant;
 KW anticoagulant; coagulant; cardiot;
 KW systemic inflammatory response syndrome; acute pancreatitis;
 KW shock syndrome; disseminated intravascular coagulation; Yeast;
 KW hyperfibrinolytic haemorrhage; myocardial infarction; 212L;
 KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
 KW allergy-induced protease release; deep vein thrombosis;
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.
 XX OS Homo sapiens.
 OS Saccharomyces cerevisiae.
 OS Synthetic.
 XX Chimeric.
 XX FH
 FT Peptide 1..51
 FT /Label= 212L_signal_peptide
 FT Cleavage-site 52..53
 FT /Label= KEX2_cleavage_site
 FT Protein 54..111
 FT /Label= HKI_18
 FT Misc-difference 62
 FT /note= "Wild-type Ser substituted by Pro"
 FT Misc-difference 64
 FT /note= "Wild-type His substituted by Thr"
 FT Misc-difference 68..70
 FT /note= "Wild-type Ala-Asp-Trp substituted by Lys-Ala-Arg"
 XX PN WO200296938-A2.
 XX PD 05-DEC-2002.
 XX PF 31-MAY-2002; 2002WO-DK000372.
 XX PR 31-MAY-2001; 2001DK-00000859.
 PR 05-JUL-2001; 2001US-0303180P.
 PA (NOVO) NOVO NORDISK AS.
 XX PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;
 XX DR WPI; 2003-041403/03.
 XX PT Kunitz-type protease inhibitor used in the treatment of inflammatory
 PT disorders.
 XX PS Example 1; Fig 8; 52pp; English.
 XX The invention relates to an isolated polypeptide comprising a 51 amino
 acid sequence being a generic sequence for a Kunitz-type protease
 inhibitor or a variant where the sequence is at least 80% identical to
 the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
 included are an isolated polypeptide obtainable by cultivation of a host
 cell comprising a polynucleotide construct encoding kunitz-type protein
 in an appropriate growth medium under conditions allowing expression of
 the polynucleotide construct and recovering the polypeptide from the
 culture medium, a polynucleotide construct encoding the kunitz-type
 protein and a host cell comprising the polynucleotide construct. The
 kunitz-type protein is used for the preparation of a medicament for the
 treatment of systemic inflammatory response syndrome, acute pancreatitis,
 shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
 haemorrhage, myocardial infarction, for prevention of blood loss during
 major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
 allergy-induced protease release, deep vein thrombosis, emphysema,
 rheumatoid arthritis, adult respiratory distress syndrome, chronic
 inflammatory bowel disease, and psoriasis. The present sequence is a
 CC mutant human HKI-18 with a yeast 212L signal peptide and a
 CC KEX2 cleavage site, expressed in yeast cells

PT disorders.
 XX
 PS Example 1; Fig 8; 52pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a 51 amino acid sequence being a generic sequence for a Kunitz-type protease inhibitor or a variant where the sequence is at least 80% identical to the Kunitz domain of human Kunitz type protease inhibitor HKI-18. Also included are an isolated polypeptide obtainable by cultivation of a host cell comprising a polynucleotide construct encoding Kunitz-type protein in an appropriate growth medium under conditions allowing expression of the polynucleotide construct and recovering the polypeptide from the culture medium, a polynucleotide construct encoding the Kunitz-type protein and a host cell comprising the polynucleotide construct. The Kunitz-type protein is used for the preparation of a medicament for the treatment of systemic inflammatory response syndrome, acute pancreatitis, shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic haemorrhage, myocardial infarction, for prevention of blood loss during major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury, allergy-induced protease release, deep vein thrombosis, embolism, inflammatory bowel disease, and psoriasis. The present sequence represents a mutant human HKI-18 with a yeast 212L signal peptide and a KEX-2 cleavage site, expressed in yeast cells
 XX
 SQ Sequence 111 AA;

Query Match 88.4%; Score 291; DB 6; Length 111;
 Best Local Similarity 89.7%; Pred. No. 7.2e-27;
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 AC AAB60623;
 KX 1 YPVRCILPPATGPCKARIIRWYFVASVQGCRGNNANPASQECMSQGS 58
 QY 54 YPVRCILPPATGSCKAWARWYFVASVQGCRGNNANPASQECMSQGS 111
 DB

RESULT 7
 AAB60623
 ID AAB60623 standard; protein; 58 AA.
 XX
 AC AAB60623;
 KX 27-APR-2001 (first entry)
 DE Human protease inhibitor BTL.010 Kunitz domain, SEQ ID No.1.
 XX
 KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor; proteinase-3 inhibitor; Kunitz domain; emphysema; idiopathic pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; platelet activation; blood coagulation; neutrophil activation; or monocytic activation; angioplasty; inflammatory disease; lung and vascular injury; nephrotropic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US6180607-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 05-AUG-1999; 99US-00369494.
 XX
 PA (DAVI/ DAVIES C.
 PA (CHEN/ CHEN D.
 PA (ROCZ/ ROCZNIK S.
 XX
 PI Davies C, Chen D, Rocznak S;
 XX
 DR WPI; 2001-120860/19.
 DR N-PSDB; AAF50750.
 XX

Query Match 88.4%; Score 291; DB 6; Length 111;
 Best Local Similarity 89.7%; Pred. No. 7.2e-27;
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 AC AAB60623;
 KX 27-APR-2001 (first entry)
 DE Human protease inhibitor BTL.010 Kunitz domain, SEQ ID No.1.
 XX
 KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor; proteinase-3 inhibitor; Kunitz domain; emphysema; idiopathic pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; platelet activation; blood coagulation; neutrophil activation; or monocytic activation; angioplasty; inflammatory disease; lung and vascular injury; nephrotropic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US6180607-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 05-AUG-1999; 99US-00369494.
 XX
 PA (DAVI/ DAVIES C.
 PA (CHEN/ CHEN D.
 PA (ROCZ/ ROCZNIK S.
 XX
 PI Davies C, Chen D, Rocznak S;
 XX
 DR WPI; 2001-120860/19.
 DR N-PSDB; AAF50750.
 XX

Query Match 88.4%; Score 291; DB 6; Length 111;
 Best Local Similarity 89.7%; Pred. No. 7.2e-27;
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 AC AAB60623;
 KX 27-APR-2001 (first entry)
 DE Human protease inhibitor BTL.010 Kunitz domain, SEQ ID No.1.
 XX
 KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor; proteinase-3 inhibitor; Kunitz domain; emphysema; idiopathic pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; platelet activation; blood coagulation; neutrophil activation; or monocytic activation; angioplasty; inflammatory disease; lung and vascular injury; nephrotropic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US6180607-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 05-AUG-1999; 99US-00369494.
 XX
 PA (DAVI/ DAVIES C.
 PA (CHEN/ CHEN D.
 PA (ROCZ/ ROCZNIK S.
 XX
 PI Davies C, Chen D, Rocznak S;
 XX
 DR WPI; 2001-120860/19.
 DR N-PSDB; AAF50750.
 XX

Query Match 88.4%; Score 291; DB 6; Length 111;
 Best Local Similarity 89.7%; Pred. No. 7.2e-27;
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 AC AAB60623;
 KX 27-APR-2001 (first entry)
 DE Human protease inhibitor BTL.010 Kunitz domain, SEQ ID No.1.
 XX
 KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor; proteinase-3 inhibitor; Kunitz domain; emphysema; idiopathic pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; platelet activation; blood coagulation; neutrophil activation; or monocytic activation; angioplasty; inflammatory disease; lung and vascular injury; nephrotropic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US6180607-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 05-AUG-1999; 99US-00369494.
 XX
 PA (DAVI/ DAVIES C.
 PA (CHEN/ CHEN D.
 PA (ROCZ/ ROCZNIK S.
 XX
 PI Davies C, Chen D, Rocznak S;
 XX
 DR WPI; 2001-120860/19.
 DR N-PSDB; AAF50750.
 XX

PT Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful for treating emphysema, cystic fibrosis, adult respiratory distress syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
 XX
 PS Claim 6; Col 9-10; 17pp; English.
 XX
 CC The invention relates to a novel human serine protease inhibitor of the Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and AAB60634). The BTL.010 protein is thought to preferentially inhibit neutral serine proteases such as elastase and proteinase-3, relative to trypsin-like and chymotrypsin-like proteases. A substantial proportion of the BTL.010 protein (AAB60631) was identified via homology searching in the GenBank high throughput genomi (HTG) DNA sequence database using the Kunitz domain sequences AAB60630, and was confirmed as being novel using the Kunitz domain sequences AAB60632, and AAB60633. This sequence information was extended to provide a larger region of the BTL.010 protein sequence data (AAB60634) by identifying an open reading frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain fragment in a 399 bp fragment of human genomic DNA (AA59750), corresponding to bases 1606-16414 of Genbank accession number AC004046. The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical compositions comprising it, may be used for inhibiting protease activity, particularly that of leukocyte elastase, in the prevention, treatment or amelioration of medical conditions such as emphysema, idiopathic pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis, compositions of the invention modulate at least one physiological condition such as platelet activation, blood coagulation, neutrophil activation, or monocytic activation. BTL.010 is also useful for the prophylactic or therapeutic treatment of patients undergoing angioplasty, and for the treatment of inflammatory diseases and diseases involving lung and vascular injury. The present sequence represents the human BTL.010 protease inhibitor Kunitz domain
 XX
 SQ Sequence 58 AA;

Query Match 80.2%; Score 264; DB 4; Length 58;
 Best Local Similarity 82.8%; Pred. No. 6.3e-24;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 AC ABG71912;
 KX 22-JAN-2003 (first entry)
 DE Human Kunitz protease inhibitor protein HKI-18.
 XX
 KW Human; protease inhibitor; kunitz; HKI-18; antiinflammatory; anticoagulant; coagulant; cardiotant; CBP; psoriasis; emphysema; systemic inflammatory response syndrome; acute pancreatitis; shock syndrome; disseminated intravascular coagulation; hyperfibrinolytic haemorrhage; myocardial infarction; cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis; allergy-induced protease release; deep vein thrombosis; adult respiratory distress syndrome; chronic inflammatory bowel disease.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 PT 5-.55
 FT /label= "This domain is claimed in claim 18"
 FT
 PN WO200296938-A2.

XX	05-DEC-2002.	PF	12-MAY-2000; 2000US-00569670.
PD		XK	
XX	31-MAY-2002; 2002WO-DK000372.	PR	05-AUG-1999; 99US-00369494.
PF		XK	
XX	31-MAY-2001; 2001DK-00000859.	PA	(FARB) BAYER PHARM CORP.
PR	05-JUL-2001; 2001US-0303180P.	XK	
XX		PI	Davies C, Chen D, Rocznak S;
PA	(NOVO) NOVO NORDISK AS.	XK	
XX		DR	
XX	Jorgensen MU, Bang S, Olsen OH, Petersen LC;	PT	WPI; 2003-041403/03.
DR	N-PSDB; ABS56455.	XK	
XX		PT	
PT	Kunitz-type protease inhibitor used in the treatment of inflammatory	XK	
XX	PT disorders.	PS	WPI; 2004-141424/14.
XX		XK	
PS	Claim 19; Fig 2; 52pp; English.	PS	New isolated polynucleotide encoding BTL.010 serine proteinase, useful
XX		XK	for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
CC	The invention relates to an isolated polypeptide comprising a 51 amino	PT	respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
CC	acid sequence being a generic sequence for a Kunitz-type protease	XK	glomerulonephritis.
CC	inhibitor or a variant where the sequence is at least 80% identical to	XX	
CC	the kunitz domain of human kunitz type protease inhibitor HKI-18. Also	PS	Claim 1; SEQ ID NO 1; 17pp; English.
CC	included are an isolated polypeptide obtainable by cultivation of a host	XK	
CC	cell comprising a polynucleotide construct encoding kunitz-type protein	CC	The invention relates to BTL.010, a human serine proteinase inhibitor of
CC	in an appropriate growth medium under conditions allowing expression of	CC	the Kunitz family and its corresponding nucleic acid sequence. The
CC	the polynucleotide construct and recovering the polypeptide from the	CC	sequences of the invention are useful for treating diseases, e.g.
CC	culture medium, a polynucleotide construct encoding the kunitz-type	CC	emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
CC	protein and a host cell comprising the polynucleotide construct. The	CC	syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC	kunitz-type protein is used for: the preparation of a medicament for the	CC	glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
CC	treatment of systemic inflammatory response syndrome, acute pancreatitis,	CC	useful for preventing neutrophil and monocyte activation and formation of
CC	shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic	CC	active oxygen species during the oxidative burst of stimulated
CC	hemorrhage, myocardial infarction, for prevention of blood loss during	CC	granulocytes. It is also useful for reducing platelet activation and
CC	major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,	CC	blood coagulation. BTL.010 DNA is useful in gene therapy. The present
CC	rheumatoid arthritis, adult respiratory distress syndrome, chronic	CC	sequence is human BTL.010 protein Kunitz domain (KD) peptide.
CC	inflammatory bowel disease, and psoriasis. The present sequence is human	XX	Sequence 58 AA;
CC	HKI-18	CC	Sequence 58 AA;
XX		CC	Query Match 80.2%; Score 264; DB 8; Length 58;
SQ	Sequence 58 AA;	CC	Best Local Similarity 82.8%; Pred. NO. 6.3e-24; Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Matched 48; Conservative 0; Gaps 0;	Db	CC	Query 1 YPVRCLIPPATPGCKARIRWYFVASVGQCNRFVYGGCGNANNFASEOBCMSQGS 58
QY 1 YPVRCLIPPATPGCKARIRWYFVASVGQCNRFVYGGCGNANNFASEOBCMSQGS 58	Db	Db 1 YPVRCLIPPATPGCKARIRWYFVASVGQCNRFVYGGCGNANNFASEOBCMSQGS 58	
RESULT 9		DB	Human HKI-18/212L signal peptide.
ADL16831		DB	Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
ADL16831 standard; peptide; 58 AA.		XX	anticoagulant; coagulant; cardiot; CSP; psoriasis; emphysema;
XX		XX	systemic inflammatory response syndrome; acute pancreatitis;
XX		XX	shock syndrome; disseminated intravascular coagulation; yeast;
XX		XX	hyperfibrinolytic haemorrhage; myocardial infarction; 212L;
XX		XX	cardiopulmonary bypass-induced pulmonary injury; rheumatoid
XX		XX	allergy-induced protease release; deep vein thrombosis;
XX		XX	adult respiratory distress syndrome; chronic inflammatory bowel disease.
DE	Human BTL.010 protein Kunitz domain (KD) peptide.	OS	Homo sapiens.
XX		OS	Saccharomyces cerevisiae.
KW	BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;	OS	Synthetic.
KW	idiopathic pulmonary fibrosis; adult respiratory distress syndrome;	XX	Chimeric.
KW	cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;	PH	
KW	inflammatory disease; oxidative burst; platelet activation;	PT	Key Peptide
KW	blood coagulation; gene therapy; human; KD.	PT	Location/Qualifiers
XX		PT	l;.51
OS		PT	/label= 212L_signal_peptide
XX	Homo sapiens.	PT	52. .53
XX	US6689582-B1.	PT	/label= KEX2_cleavage_site
XX		PT	54. .111
PD	10-FEB-2004.	PT	/label= HKI_18
XX		PN	WO200295938-A2.

KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KW inflammatory disease; oxidative burst; platelet activation;
 KW blood coagulation; gene therapy.
 OS Unidentified.
 XX
 PH Key
 FT Domain
 PT /note = Kunitz domain
 XX
 PN US6689582-B1.
 XX
 PD 10-FEB-2004.
 XX
 PP 12-MAY-2000; 2000US-00569670.
 XX
 PR 05-AUG-1999; 99US-0036994.
 XX
 PA (FARB) BAYER PHARM CORP.
 XX
 PT Davies C, Chen D, Rocznak S;
 XX
 DR WPI; 2004-141424/14.
 XX
 PT New isolated polynucleotide encoding BTL 010 serine proteinase, useful
 PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
 PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
 PT glomerulonephritis.
 XX
 PS Disclosure; SEQ ID NO 15; 17pp; English.
 XX
 CC The invention relates to BTL 010, a human serine proteinase inhibitor of
 CC the Kunitz family and its corresponding nucleic acid sequence. The
 CC sequences of the invention are useful for treating diseases, e.g.
 CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
 CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
 CC glomerulonephritis or inflammatory diseases. The BTL 010 protein is also
 CC useful for preventing neutrophil and monocyte activation and formation of
 CC active oxygen species during the oxidative burst of stimulated
 CC granulocytes. It is also useful for reducing platelet activation and
 CC blood coagulation. BTL 010 DNA is useful in gene therapy. The present
 CC sequence is a BTL 010 protein related protein.
 XX
 SQ Sequence 189 AA;
 Query Match 80.2%; Score 264; DB 8; Length 189;
 Best Local Similarity 82.8%; Pred. No. 2.1e-23; Mismatches 10; Indels 0; Gaps 0;
 Matches 48; Conservative 0; MisMatches 10; Indels 0; Gaps 0;
 Oy 1 YPVRCLIPPAPEGPCKARIIRWYFVASVQCNRFVYGGCRNANNFASEBCMSSCGS 58
 Db 688 YPVRCLIPPAEHPCKARIIRWYFVASVQCNRFVYGGCRNANNFASEBCMSSCGS 745
 Sequence 1235 AA;
 Query Match 80.2%; Score 264; DB 8; Length 1235;
 Best Local Similarity 82.8%; Pred. No. 1.4e-22; Mismatches 10; Indels 0; Gaps 0;
 Matches 48; Conservative 0; MisMatches 10; Indels 0; Gaps 0;
 Oy 1 YPVRCLIPPAPEGPCKARIIRWYFVASVQCNRFVYGGCRNANNFASEBCMSSCGS 58
 Db 688 YPVRCLIPPAEHPCKARIIRWYFVASVQCNRFVYGGCRNANNFASEBCMSSCGS 745
 RESULT 14
 ABR58408
 ID ABR58408 standard; protein; 1280 AA.
 XX
 AC ABR58408;
 XX
 DT 07-JUL-2003 (first entry)
 DE Human Nov2a.
 XX
 KW Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cyrostatic; nootropic; neuroprotective; dialipidaemia;
 KW antiparkinsonian; antilipaemic; gene therapy; metabolic disorder;
 KW diabetes; obesity; infection; cachexia; cancer; Parkinson's disease;
 KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
 KW haematopoietic disorder.
 DT Homo sapiens.
 XX
 DE Protein #48 with increased gene expression in renal cell carcinoma.
 XX
 DE
 KW Cytostatic; gene therapy; differential expression; renal cell carcinoma;
 KW clear cell RCC; papillary RCC; chromophobe/oncocytoma RCC;
 KW sarcomatoid RCC; TCC; Wilms' tumor; gene expression; kidney cancer;
 KW diagnostic marker; cancer.
 OS Homo sapiens.
 XX
 PN WO2004032842-A2.

PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 22-OCT-2001; 2001US-0341056P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 28-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 12-APR-2002; 2002US-0371972P.
 PR 12-APR-2002; 2002US-0371980P.
 PR 17-APR-2002; 2002US-0373261P.
 PR 19-APR-2002; 2002US-037305P.
 PR 23-APR-2002; 2002US-0374738P.
 PR 16-MAY-2002; 2002US-0381101P.
 PR 17-MAY-2002; 2002US-0381635P.
 PR 20-MAY-2002; 2002US-0383830P.
 PR 20-OCT-2002; 2002US-0383830P.
 PR 20-OCT-2002; 2002US-00262839.
 PA (CURA-) CURAGEN CORP.
 XX
 Alisobrook JP, Andersen DW, Boldog FL, Burgess CB, Catterton E, Eisinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W, Kekuda R, Leach MD, Li L, Miller CR, Patturajan M, Rieger DK, Rothberg ME, Shimkets RA, Smithson G, Spytek KA, Taupier RJ, Vernet CAM, Voss EZ, Zernhusen BD, Zhong M;
 DR N-PSDB; ACT72120.
 XX
 NOV polypeptides and nucleic acids useful for diagnosing, preventing or treating NOV-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 WPI; 2003-381625/36.
 XX
 PI DAVIES C.
 PI (CHEN) CHEN D.
 PI (ROCZ) ROCZNIK S.
 PA
 Davies C, Chen D, Rocznak S;
 DR N-PSDB; AAF59750.
 PR
 Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful for treating emphysema, cystic fibrosis, adult respiratory distress syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
 PR Disclosure; Col 5-6; 17pp; English.
 PS
 The invention relates to a novel human serine protease inhibitor of the Kunitz family, BTL.010. Fragments given in AAB60633, AAB60631 and AAB60634. The BTL.010 protein is thought to preferentially inhibit neutral serine proteases such as elastase and proteinase-3, relative to trypsin-like and chymotrypsin-like proteases. A substantial proportion of the BTL.010 protein Kunitz domain (AAB60631) was identified via homology searching in the Genbank high throughput genomic (HTG) DNA sequence database using the Kunitz domain sequences AAB60630, and was confirmed as being novel using the Kunitz domain sequences AAB60632, and AAB60633. This sequence information was extended to provide a larger region of BTL.010 protein sequence data (AAB60634) by identifying an open reading frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain fragment in a 399 bp fragment of human genomic DNA (AAB59750), corresponding to bases 15016-16141 of GenBank accession number AC004446. The entire BTL.010 Kunitz domain sequence (AAB6063) was obtained from the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical compositions comprising it, may be used for inhibiting protease activity, particularly that of leukocyte elastase, in the prevention, treatment or amelioration of medical conditions such as emphysema, idiopathic pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010 compositions of the invention modulate at least one physiological condition such as platelet activation, blood coagulation, neutrophil activation, or monocyte activation. BTL.010 is also useful for the prophylactic or therapeutic treatment of patients undergoing angioplasty, and for the treatment of inflammatory diseases and diseases involving lung and vascular injury. The present sequence represents a substantial proportion of the human BTL.010 protease inhibitor Kunitz domain
 XX
 SQ Sequence 1280 AA;
 SQ Query Match 80.2%; Score 264; DB 6; Length 1280;
 Best Local Similarity 82.8%; Pred. No. 1.4e-22;
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 YPVRCLIPATPCKARIRWYFVASVQCNRPFVYGGCRGNANNFASBOECMSSQ 58
 Db 752 YPVRCLIPATPCKARIRWYFVASVQCNRPFVYGGCRGNANNFASBOECMSSQ 809
 SQ Sequence 51 AA;
 SQ Query Match 67.0%; Score 220.5; DB 4; Length 51;
 Best Local Similarity 80.8%; Pred. No. 8.7e-19;
 Matches 42; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
 QY 5 CLIPATPCKARIRWYFVASVQCNRPFVYGGCRGNANNFASBOECMSSQ 56
 Db 1 CLIPATPCKARIRWYFVASVQCNRPFVYGGCRGNANNFASBOECMSSQ 51
 DB Human protease inhibitor BTL.010 Kunitz domain fragment, SEQ ID NO:9.
 XX Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;
 KW protease-3 inhibitor; Kunitz domain; emphysema;
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:48:01 ; Search time 16 Seconds
 (without alignments)
 348.786 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329

Sequence: 1 YPVRCILPPATGPKKARIK.....RGANNFASEQECMSCCQGS 58

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : PIR 79;*

1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGMENTS

RESULT 1

TBO

basic proteinase inhibitor precursor - bovine

N Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallikre

C Species: Bos primigenius taurus (cattle)

C Date: 24-Apr-1984 #Sequence revision 22-Jul-1994 #text change 09-Jul-2004

C Accession: S00277; A30333; S05456; S02486; S28197; A90162; A92023; A90736; A90927; A346

R Creighton, T.B.; Charles, I.G. J. Mol. Biol. 194, 11-22, 1987

A Title: Sequences of the genes and polypeptide precursors for two bovine protease inhibi

A Reference number: S00274; MUID:87283904; PMID:2441071

A Molecule type: DNA; mRNA

A Residues: 1-100 <CII>

A Cross-references: UNIPROT: P00974; GB:M20934; GB:X05274; NID:9162767; PIDN:AAD13685.1; I

R Creighton, T.B.; Charles, I.G. Cold Spring Harb Symp. Quant. Biol. 52, 511-519, 1987

A Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.

A Reference number: S00277; MUID:88295740; PMID:2456884

A Accession: A30333

A Molecule type: DNA

A Residues: 1-100 <CII>

A Cross-references: GB:M20934; GB:X05274; NID:9162767; PIDN:AAD13685.1; PID:9162769

R Creighton, T.B.; Anderson, S. Biochem. J. 233, 443-450, 1986

A Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic er

A Reference number: S10546; MUID:8615874; PMID:2420326

A Accession: S10546

A Molecule type: DNA

A Residues: 34-97 <KIN>

R Pioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.

Bio. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988

A Title: Aprotinin-like isoInhibitors in bovine organs.

A Residues: 36-93 <PRO>

R Ikekita, M.; Jone, C.S.; Kamo, M.; Tsubgita, A.; Kizuki, K.; Moriya, H.

Protein Seq. Data Anal. 5, 7-11, 1992

A Title: Purification and characterization of the major cationic kallikrein inhibitor in

A Reference number: S28197; MUID:9315003; PMID:1283464

A Accession: S28197

A Molecule type: protein

A Residues: 36-93 <PRO>

R Kassell, B.; Iaskoski, M.

Biochem. Biophys. Res. Commun. 20, 463-468, 1965

A Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.

A Reference number: A90162; MUID:66083012; PMID:5860161

A Contents: annotation; disulfide bonds

A Accession: A90162

A Molecule type: protein

A Residues: 36-93 <KAS>

alpha-1-microglobu
 venom, basic protei
 alpha-1-microglobu
 alpha-1-microglobu
 alpha-1-microglobu
 trypsin inhibitor,
 Kunitt-type protei
 venom basic protei
 tissue factor path
 protein C3/C3-6a [
 hypothetical prote
 tissue factor path
 alpha-1-microglobu
 hypothetical prote
 venom basic protei
 tissue factor path

R;Andresser, F.A.; Hornig, S.
J. Biol. Chem. 241, 1568-1572, 1966
A;Title: The disulfide linkages in kallikrein inactivator of bovine lung.
A;Reference number: A92023; MUID:66171231; PMID:5296424
A;Accession: A92023
A;Molecule type: protein
A;Residues: 36-93 <AN2>
R;Chauvet, J.; Achér, R.
Bull. Soc. Chim. Biol. 49, 985-1000, 1967
A;Title: La structure covalente d'un inhibiteur polypeptidique de la trypsin (inhibiteur
A;Reference number: A90736; MUID:68012003; PMID:603284
A;Contents: annotation; disulfide bonds
A;Accession: A90736
A;Molecule type: protein
A;Residues: 36-93 <CHA>
R;Dlouha, V.; Pospisilova, D.; Meloun, B.; Sorm, F.
Collect. Czech. Chem. Commun. 33, 1263-1265, 1968
A;Title: Sequence of residues 18-20 in pancreatic trypsin inhibitor.
A;Reference number: A90927
A;Residues: 36-93 <DPO>
R;Huber, R.; Kukla, D.; Rühlmann, A.; Epp, O.; Formanek, H.
Naturforsch 57, 339-392, 1970
A;Title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and confc
A;Reference number: A93410; MUID:70255230; PMID:5477861
A;Contents: annotation; X-ray crystallography of basic protease inhibitor, 2.5 angstrom
R;Lewis, R. V.; Ray, P.; Coguill, R.; Kruegel, W.
Biochem. Biophys. Res. Commun. 167, 543-547, 1990
A;Title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells.
A;Reference number: A34658; MUID:90211226; PMID:2322242
A;Accession: A34658
A;Molecule type: protein
A;Residues: 36-53, 55-81 <NEW>
R;Anderson, S.; Kingston, I.B.
Proc. Natl. Acad. Sci. U.S.A. 80, 6338-6342, 1983
A;Title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a
A;Reference number: A93977; MUID:84070725; PMID:6580617
A;Accession: A93977
A;Molecule type: protein
A;Residues: PSLNRDPPIPA, 34-97, 'GKIGGRAGEGKG' <AND>
A;Cross-references: GB:X03365; GB:K01966; NID:9142; PRDB:CAA27062.1; PID:91364183
R;Siemann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A;Title: Characterization and sequence determination of six aprotinin homologues from bov
A;Reference number: S00371; MUID:88221840; PMID:2453200
A;Accession: S1062
A;Molecule type: protein
A;Residues: 36-66, 'P', 68-82, 'S', 84-93 <SIB>
A;Experimental source: lung
A;Note: the authors designated this protein as isoaprotinin 2
C;Comment: Basic proteinase inhibitor is an intracellular polypeptide found in many tiss
C;Genetics: Intron: 34/1; 98/1
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-35/Domain: propeptide #status predicted <PRO>
F;36-60/Domain: basic proteinase inhibitor #status experimental <MAT>
F;40-90/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;50/Inhibitory site: Lys (trypsin, chymotrypsin, kallikrein, plasmin) #status experimen
Query Match 58.4%; Score 192; DB 1; Length 100;
Best Local Similarity 57.9%; Pred. No. 2 5e-16;
Matches 33; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

RESULT 2
S00371
Isoaprotinin G2 - bovine hybrid
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S00371
R;Siekmann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A;Title: Characterization and sequence determination of six aprotinin homologues from bov
A;Reference number: S00371; MUID:88221840; PMID:2453200
A;Accession: S1063
A;Molecule type: protein
A;Residues: 1-58 <SIB>
A;Cross-references: UNIPROT:Q9M312
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;15-55/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;15/Inhibitory site: Lys (trypsin) #status predicted
Query Match 57.1%; Score 188; DB 2; Length 58;
Matches 32; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
Qy 2 PVRCLLPPATGCKKARIRWYFASVQCNRRTYGGCRGNNFASQCMSSCGS 58
Db 2 PDCLEPPYTGCKKARIRWYFASVQCNRRTYGGCRGNNFASQCMSSCGS 58
RESULT 4
TIBOR
serum basic proteinase inhibitor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004
C;Accession: A01206
R;Wachter, E.; Depner, K.; Hochstrasser, K.; Lempart, K.; Geiger, R.
FEBS Lett. 119, 58-62, 1980
A;Title: A new Kunitz-type inhibitor from bovine serum amino acid sequence determination.
A;Reference number: A01206; MUID:81044408; PMID:7428928
A;Accession: A01206
A;Molecule type: protein
A;Residues: 1-60 <WAC>
A;Cross-references: UNIPROT:R00975
C;Comment: This inhibitor has activity very similar to that of the basic protease inhibit
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog

C:Keywords: serine proteinase inhibitor
 F:7-5/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:7/Inhibitory site: Lys (trypsin) #status experimental

Query Match 55.9%; Score 184; DB 1; Length 60;
 Best Local Similarity 54.4%; Pred. No. 1; Se-15;
 Matches 31; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
 Qy 2 PVRCLLPPATGPKKARIRWYFVASVGCNRFVYGGCRGNANNFASEBCMSSCOGS 58
 Db 4 PDRCLEPPYTGPKKAMIRYFVYKAGFCETFVYGGCRKSNNFKSABDCMRTCGGA 60

RESULT 5

TB0SP spleen basic proteinase inhibitor precursor - bovine
 N:Alternate names: Isoprolin 1
 C:Species: Bos primigenius taurus (cattle)
 C;Date: 07-sep-1990 #sequence_revision 22-jul-1994 #text_change 09-jul-2004
 C;Accession: S02724; B30333; A27417; S02487; S10547; S13478; A23915; S10064
 R;Crichton, T.B.; Charles, I.G.
 J. Mol. Biol. 194, 11-22, 1987
 A;Title: Sequences of the genes and polypeptide precursors for two bovine protease inhibitor
 A;Reference number: S00274; MUID:87283904; PMID:2441071
 A;Accession: S0374
 A;Molecule type: DNA; mRNA
 A;Residues: 1-100 <CR>
 A;Cross-references: UNIPROT:P04815; EMBL:X05275; NID:9163718; PIDN:AAA51418_1; PID:91637
 R;Creighton, T.E.; Charles, I.G.
 Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
 A;Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.
 A;Reference number: A50926; MUID:88259740; PMID:2456884
 A;Accession: B30333
 A;Molecule type: DNA
 A;Residues: 1-100 <CRE>
 A;Cross-references: GB:M20335; GB:X05275; NID:9163718; PIDN:AAA51418_1; PID:9163720
 R;Barra, D.; Simmaco, M.; Bossa, F.; Fioretti, E.; Angeletti, M.; Ascoli, F.
 J. Biol. Chem. 262, 13916-13919, 1987
 A;Title: Primary structure of a protease inhibitor from bovine spleen. A possible int
 A;Reference number: A27417; MUID:88007630; PMID:3654647
 A;Molecule type: protein
 A;Residues: 34-99 <BAR>
 A;Note: the more abundant form of isoform I lacks 99-Asn
 R;Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
 Biol. Chem. Hoppe-Seyler 359(Suppl.), 37-42, 1988
 A;Title: Aprotinin-like isoform I from bovine organs.
 A;Reference number: S02485; MUID:89076531; PMID:2462435
 A;Accession: S02487
 A;Molecule type: protein
 A;Residues: 34-99 <FO>
 R;Kingston, I.B.; Anderson, S.
 Biochem. J. 233, 443-450, 1986
 A;Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic e
 A;Reference number: S10546; MUID:86158754; PMID:2420326
 A;Accession: S10547
 A;Molecule type: DNA
 A;Residues: 34-97 <KIN>
 R;Barra, D.; Fioretti, E.; Angeletti, M.; Maras, B.; Bossa, F.; Ascoli, F.
 Biophys. Acta 1076, 143-147, 1991
 A;Title: Proteinase isoform I from bovine spleen: primary structure of an intermedia
 A;Reference number: S13478; MUID:91098258; PMID:198787
 A;Accession: S13478
 A;Molecule type: protein
 A;Residues: 36-97 <BA2>
 R;Fioretti, E.; Iacopino, G.; Angeletti, M.; Barra, D.; Bossa, F.; Ascoli, F.
 J. Biol. Chem. 260, 11451-11455, 1985
 A;Reference number: A23915; MUID:86008178; PMID:2413011
 A;Accession: A23915
 A;Molecule type: protein
 A;Residues: 36-93 <FI2>
 R;Siekmann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
 A;Note: three disulfide bonds are present

RESULT 6

AS5115
 bovine plasmin/trypsin inhibitor - pig
 C:Species: Sub scrofa domestica (domestic pig)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A55115
 R;Stallings-Mann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
 J. Biol. Chem. 269, 24090-24094, 1994
 A;Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase inhibitor
 A;Reference number: A55115; MUID:95014140; PMID:7939061
 A;Accession: A55115
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-122 <STR>
 A;Cross-references: UNIPROT:Q29100; GB:L14282; NID:9682652; PIDN:AAA62425_1; PID:9682653
 A;Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Arg
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C:Keywords: serine proteinase inhibitor
 F:38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 52.9%; Score 174; DB 1; Length 122;
 Best Local Similarity 51.9%; Pred. No. 4; Se-14;
 Matches 28; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 Qy 2 PVRCLLPPATGPKKARIRWYFVASVGCNRFVYGGCRGNANNFASEBCMSSCOGS 55
 Db 35 PGFCREPPYTGPKCSAHFRVIFNATIGLCQSFVYGGCRKSNNFKSABDCMRTCGGA 88

RESULT 7

S41082
 amyloid precursor protein homolog - human (fragment)
 C:Species: Homo sapiens (man)
 C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C;Accession: S41082
 R;Petersen, L.C.; Bjorn, S.B.; Norris, F.; Norris, K.; Sprecher, C.; Foster, D.C.
 FEBS Lett. 338, 53-57, 1994
 A;Title: Expression, purification and characterization of a Kunitz-type protease inhibitor
 A;Reference number: S41082; MUID:94139895; PMID:8307156
 A;Accession: S41082
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-111 <P6T>
 A;Cross-references: UNIPROT:Q7M4L3
 F;59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match
 Best Local Similarity 51.1%; Score 168; DB 2; Length 111;
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
 Db 59 CSQEA
 Qy 5 CLPPATGPKCARIIRWYFVASVQCNRFVYGGCRGNANNFASEQECMSQQ 56
 C;Species: Mus musculus (house mouse)
 C;Accession: A49974 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 R;Slunt, H.H.; Thirukaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
 J. Biol. Chem. 269, 2637-2644, 1994
 A;Title: Expression of a ubiquitously cross-reactive homologue of the mouse beta-amyloid
 A;Reference number: A49974; MUID:94132029; PMID:830594
 A;Accession: A49974
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-751 <SLU>
 A;Cross-references: UNIPROT:Q60709; GB:U15571; NID:9558467; PIDN:AAA50603.1; PID:g558468
 A;Note: sequence extracted from NCBP backbone (NCBP:14635)
 F;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 51.1%; Score 168; DB 2; Length 751;
 Best Local Similarity 55.8%; Pred. No. 1.4e-12;
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
 Qy 5 CLPPATGPKCARIIRWYFVASVQCNRFVYGGCRGNANNFASEQECMSQQ 56
 Db 310 CSQEA
 Qy 5 CLPPATGPKCARIIRWYFVASVQCNRFVYGGCRGNANNFASEQECMSQQ 56
 Db 310 CSQEA
 RESULT 9
 A49321
 amyloid beta (A1) homolog 2 precursor - human
 N;Alternate names: CDEI-binding protein
 C;Species: Homo sapiens (man)
 C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A49321; S34644; S34645
 R;Sprcher, C.A.; Grant, R.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, B.; Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for alternative splicing
 A;Reference number: A49321; MUID:93250009; PMID:8485127
 A;Accession: A49321
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-765 <SLR>
 A;Cross-references: UNIPROT:Q06481; GB:S60099; NID:9300168; PIDN:MAC60589.1; PID:g300169
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBP backbone (NCBN:131198; NCBP:131199)
 A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
 R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
 A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor protein homolog 2 precursor
 A;Reference number: S34644
 A;Accession: S34644
 A;Molecule type: mRNA
 A;Residues: 1-763 <VON>
 A;Cross-references: EMBL:222572; NID:9394763; PIDN:CAA80295.1; PID:g394764
 R;Waco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.; Nature Genet. 5, 95-99, 1993
 A;Title: Isolation and characterization of APP2 encoding a homologue of the Alzheimer's disease amyloid precursor protein
 A;Reference number: S40519; MUID:94035131; PMID:8220455
 RESULT 8
 A49974
 beta-amyloid precursor protein 2 homolog APLP2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: A49974 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 R;Slunt, H.H.; Thirukaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
 J. Biol. Chem. 269, 2637-2644, 1994
 A;Title: Expression of a ubiquitously cross-reactive homologue of the mouse beta-amyloid
 A;Reference number: A49974; MUID:94132029; PMID:830594
 A;Accession: A49974
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-751 <SLU>
 A;Cross-references: UNIPROT:AAA50603.1; PID:g558468
 A;Note: sequence extracted from NCBP backbone (NCBP:14635)
 F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 51.1%; Score 168; DB 2; Length 751;
 Best Local Similarity 55.8%; Pred. No. 1.4e-12;
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
 Db 59 CSQEA
 Qy 5 CLPPATGPKCARIIRWYFVASVQCNRFVYGGCRGNANNFASEQECMSQQ 56
 Db 310 CSQEA
 RESULT 10
 A49280
 amyloid precursor-like protein - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S42880; S47282
 R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
 submitted to the EMBL Data Library, March 1994
 A;Description: Complete nucleotide and deduced amino acid sequence of rat amyloid precursor protein homolog 2 precursor
 A;Reference number: S42880
 A;Accession: S42880
 A;Molecule type: mRNA
 A;Residues: 1-765 <RAN>
 A;Cross-references: UNIPROT:P15943; EMBL:X77934
 R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
 Biochem. Biophys. Acta 1219, 167-170, 1994
 A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor
 A;Reference number: S47528; MUID:94368849; PMID:8086458
 A;Accession: S47528
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-765 <RAN>
 A;Cross-references: EMBL:X77934
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology <BPI>
 F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 51.1%; Score 168; DB 2; Length 765;
 Best Local Similarity 55.8%; Pred. No. 1.4e-12;
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
 Db 59 CSQEA
 Qy 5 CLPPATGPKCARIIRWYFVASVQCNRFVYGGCRGNANNFASEQECMSQQ 56
 Db 312 CSQEA
 RESULT 11
 TIVITI
 venom basic proteinase inhibitor I - western sand viper
 N;Alternate names: venom trypsin inhibitor I
 C;Species: Vipera ammodytes ammodytes (western sand viper)
 C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
 C;Accession: A01222
 R;Riconja, A.; Melon, B.; Gibensem, F.
 Biochim. Biophys. Acta 748, 429-445, 1983
 A;Title: The primary structure of Vipera ammodytes venom trypsin inhibitor I.
 A;Reference number: A01222; MUID:84053385; PMID:663951
 A;Accession: A01222
 A;Molecule type: protein
 A;Residues: 1-61 <RIT>
 A;Cross-references: UNIPROT:P00991

C:Comment: This protein inhibits trypsin and kallikrein.
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C:Keywords: pyroglutamic acid; serine proteinase inhibitor; venom
 C:Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:1/Modified site: Pyroglutamine carboxylic acid (Gln) #status experimental
 F:7-57/16-40,32-33/Dsulfide bonds: #status predicted

RESULT 12

Query Match 49.8%; Score 164; DB 1; Length 61;
 Best Local Similarity 48.3%; Pred. No. 4.2e-13; Mismatches 20; Indels 0; Gaps 0;
 Matches 28; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 YPVRCLLPPATGCKKARIRWYFVASVQCNRFVYGGCRGNANNFASEQCMSSCG 57
 Db 3 HPKFCYCLPADPGRCKAHIPRFYDSDASNKCNKFYIGJCPGNANNFKTWDCECRQTCGAS 60

basic proteinase inhibitor - great pond snail
 NJ:Alternate names: trypsin inhibitor
 C:Species: *Lymnaea stagnalis* (great pond snail)
 C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
 C:Accession: A59204

R:Nagle, G.
 Submitted to the Protein Sequence Database, March 2000
 A:Description: *Lymnaea* trypsin inhibitor.
 A:Reference number: A59204
 A:Accession: A59204

A:Residues: 1-57 <NAG>
 A:Cross-references: UNIPROT:Q7M411
 A:Experimental source: albumen gland
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C:Keywords: glycoprotein; serine proteinase inhibitor
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:5-55,14-38,30-51/Dsulfide bonds: #status predicted
 F:15/Inhibitory site: Lys (trypsin) #status predicted
 F:24/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 49.5%; Score 163; DB 2; Length 57;
 Best Local Similarity 49.0%; Pred. No. 5.2e-13; Mismatches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
 Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 5 CLIPPATGCKKARIRWYFVASVQCNRFVYGGCRGNANNFASEQCMSSCG 55
 Db 5 CSUPSERGCKSKFLRHYNSINACDSFVYGGCKGNANNFKDIDCKAC 55

RESULT 13

Query Match 49.5%; Score 163; DB 2; Length 57;
 Best Local Similarity 48.3%; Pred. No. 4.2e-13; Mismatches 20; Indels 0; Gaps 0;
 Matches 28; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 YPVRCLLPPATGCKKARIRWYFVASVQCNRFVYGGCRGNANNFASEQCMSSCG 57
 Db 3 HPKFCYCLPADPGRCKAHIPRFYDSDASNKCNKFYIGJCPGNANNFKTWDCECRQTCGAS 60

basic proteinase inhibitor - loggerhead
 NJ:Alternate names: Caretta caretta (loggerhead)
 C:Species: *Caretta caretta* (loggerhead)
 C:Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
 C:Accession: A01224

R:Kato, I.; Tominaga, N.
 Fed. Proc. 38, 832, 1979

A:Title: Trypsin--subtilisin inhibitor from red sea turtle eggwhite consists of two tandem
 A:Reference number: A01224
 A:Accession: A01224

A:Molecule type: protein
 A:Residues: 1-110 <KAT>
 A:Cross-references: UNIPROT:PO0993
 C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domains
 C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor
 C:Keywords: pyroglutamic acid; serine proteinase inhibitor
 F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:63-105/Domain: antileukoproteinase repeat homology <ALP>
 F:1/Modified site: Pyroglutamine carboxylic acid (Gln) #status experimental
 F:8-58,17-1,33-54,67-93,76-97,80-92,86-101/Dsulfide bonds: #status predicted

Query Match 49.5%; Score 163; DB 1; Length 110;
 Best Local Similarity 48.1%; Pred. No. 9.5e-13; Mismatches 25; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
 Matches 25; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 5 CLIPPATGCKKARIRWYFVASVQCNRFVYGGCRGNANNFASEQCMSSCG 56
 Db 8 CRUPPAGTGCCKKIPRFYNPASRMCEPSFGCKGNANNFKTAKACVACR 59

RESULT 14

Query Match 49.5%; Score 163; DB 1; Length 110;
 Best Local Similarity 48.1%; Pred. No. 9.5e-13; Mismatches 25; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
 Matches 25; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 5 CLIPPATGCKKARIRWYFVASVQCNRFVYGGCRGNANNFASEQCMSSCG 56
 Db 8 CRUPPAGTGCCKKIPRFYNPASRMCEPSFGCKGNANNFKTAKACVACR 59

hypothetical protein R12A1.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T32060

R:Pauley, A.; Andrews, S.
 Submitted to the EMBL Data Library, July 1997

A:Description: The sequence of *C. elegans* cosmid R12A1.
 A:Reference number: 22118

A:Accession: T32060

A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-249 <PAU>
 A:Cross-references: UNIPROT:O16701; EMBL:AF016680; PIDN:AAB66164.1; GSPDB:GN00023; CESP:R12A1.3
 A:Experimental source: strain Bristol N2; clone R12A1
 C:Genetics:
 A:Gene: CEBP:R12A1.3
 A:Map position: 5
 A:Introns: 75/1; 139/1

Query Match 48.9%; Score 161; DB 2; Length 249;
 Best Local Similarity 55.6%; Pred. No. 3.5e-12; Mismatches 30; Conservative 8; Mismatches 12; Indels 4; Gaps 1;
 Matches 30; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

Qy 5 CLIPPATGCKKARIRWYFVASVQCNRFVYGGCRGNANNFASEQCMSSCG 58
 Db 143 CSPLAVGSCATPARYDSSGRCQWMSGCGANNFQSS---LSSCGT 192

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
 C:Keywords: serine proteinase inhibitor; venom
 C:Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 49.5%; Score 163; DB 2; Length 62;
 Best Local Similarity 50.0%; Pred. No. 5.6e-13; Mismatches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
 Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Search completed: August 25, 2005, 04:55:46
 Job time : 1.7 secs

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GENERAL INFORMATION:

APPLICANT: Bjorn, Soeren E.

APPLICANT: No. 5591603ris, Kjeld

APPLICANT: Dines, Viggo

APPLICANT: No. 5591603ris, Fanny

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5591603ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: Christensen, Niels D.

TITLE OF INVENTION: Process for the Preparation of Aprotinin

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:

ADDRESSE: No. 5591603 No. 5591603disk of No. 5591603th America, Inc.

STREET: 405 Lexington Avenue, 62nd Floor

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STATE: New York

COUNTRY: United States of America

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/084,718

FILING DATE: 19930623

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 4501/87

FILING DATE: 28-AUG-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/084,718

FILING DATE: 19930623

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 2254/88

FILING DATE: 26-APR-1988

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK88/00138

FILING DATE: 28-AUG-1988

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK89/00096

FILING DATE: 25-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 2254/88

FILING DATE: 26-APR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/466,408

FILING DATE: 21-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 2361/90

FILING DATE: 01-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/598,337

FILING DATE: 19-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 1118/91

FILING DATE: 12-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK91/00299

FILING DATE: 01-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,687

FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/024,925

FILING DATE: 26-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: AGT1B, Cherry H.

REGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 3143.224-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-867-0398

INFORMATION FOR SEQ ID NO: 75:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-084-718-75

Query Match: 63.2%; Score 208; DB 1; Length 109;

Best Local Similarity: 63.0%; Pred. No. 2.6e-18;

Matches: 34; Conservative: 8; Mismatches: 12; Indels: 0; Gaps: 0;

QY 5 CLUPPATGPKCKARIIRVWVAVSGQCNRPVIGCRGNANNFASEQBOMSSCGS 58

DO 56 CLERPPSTGPKCKARIIRVYFNAKAGLCTTFVGGCRGNGNNFKSAEDCMTCCGA 109

RESULT 8
US-08-084-718-75

Sequence 75, Application US/08443976

Patent No. 5618915

GENERAL INFORMATION:

APPLICANT: Bjorn, Soeren E.

APPLICANT: No. 5618915ris, Kjeld

APPLICANT: Dines, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

APPLICANT: No. 5618915rskov-Lauritsen, Leif

APPLICANT: Christensen, Niels D.

APPLICANT: Bregenaard, Claus

APPLICANT: No. 5618915ris, Fanny

APPLICANT: Petersen, Lars C.

APPLICANT: No. 5618915ris, Viggo

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/084,718
 FILING DATE: 19930623
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 4501/87
 FILING DATE: 28-AUG-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2254/88
 FILING DATE: 26-APR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK88/00138
 FILING DATE: 28-AUG-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2254/88
 FILING DATE: 26-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/466,408
 FILING DATE: 21-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2361/90
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/598,337
 FILING DATE: 19-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 1118/91
 FILING DATE: 12-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00299
 FILING DATE: 01-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Agris, Cheryl H.
 REGISTRATION NUMBER: 34,086
 FILING DATE: 29-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/024,925
 FILING DATE: 26-FEB-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,687
 FILING DATE: 12-JUN-1992
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 S-08-084-718-59
 Query Match 61.7% Score 203; DB 1; Length 111;
 Best Local Similarity 59.6%; Pred. No. 1.1e-17; Indels 0; Gaps 0;
 Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 2 PVRCLLPPATGPCKARIRKIRWVAVSGVGQCRFVTCGCRGNANNFASEQECMSSCGS 58
 55 PDRCLEPSPGCKARIRKIRFYDATAGLCSTFVVGCCRANRNNFGSAEDCMECTCGA 111
 S-08-084-718-59
 Sequence 59, Application US/08443976
 Patent No. 5618915
 GENERAL INFORMATION:
 APPLICANT: Bjorn, Soeren E.
 APPLICANT: No. 5618915ris, Kjeld
 APPLICANT: Dineb, Viggo
 APPLICANT: No. 5618915rskov-Lauritsen, Leif
 S-08-084-43-976-59
 Sequence 59, Application US/08443976
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,976
 FILING DATE: 18-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/084,718
 FILING DATE: 23-JUN-1993
 APPLICATION NUMBER: PCT/DK88/00138
 FILING DATE: 28-AUG-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK89/00096
 FILING DATE: 26-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/466,408
 FILING DATE: 21-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2361/90
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/598,337
 FILING DATE: 19-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 1118/91
 FILING DATE: 12-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00299
 FILING DATE: 01-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,687
 FILING DATE: 12-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00299
 FILING DATE: 01-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/024,925
 FILING DATE: 26-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Agris, Cheryl H.
 REGISTRATION NUMBER: 34,086
 REFERENCE/DOCKET NUMBER: 3143.224-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-443-976-59

Query Match 61.7%; Score 203; DB 1; Length 111;
 Best Local Similarity 59.6%; Pred. No. 1.1e-17;
 Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 Qy 2 PVRCLLPPATGCKARIRWYFVASVSGCQNRFVYGGCRGNNFASSEQMSQCGS 58
 Db 55 PDCFCLSPPTGCKARIRWYFVASVSGCQNRFVYGGCRGNNFASSEQMSQCGS 58

RESULT 12
 US-08-443-977-59
 ; Sequence 59, Application US/08443977
 ; GENERAL INFORMATION:
 ; APPLICANT: Bjorn, Soeren E.
 ; APPLICANT: No. 5621074ris, Kjeld
 ; APPLICANT: Dinesb, Viggo
 ; APPLICANT: No. 5621074risbckov-Lauritsen, Leif
 ; APPLICANT: Christensen, Niels D.
 ; APPLICANT: Bregenbaard, Claus
 ; APPLICANT: No. 5621074ris, Fanny
 ; TITLE OF INVENTION: Process for the Preparation of Aprotinin
 ; NUMBER OF SEQUENCES: 83
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: No. 56210740 No. 5621074disk of No. 5621074th America, Inc.
 ; STREET: 405 Lexington Avenue, 62nd Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/443,977
 ; FILING DATE: 18-MAY-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/084,718
 ; FILING DATE: 23-JUN-1993
 ; APPLICATION NUMBER: US/08/443,977
 ; FILING DATE: 18-MAY-1987
 ; APPLICATION NUMBER: DK 2254/88
 ; FILING DATE: 26-APR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DK88/00138
 ; FILING DATE: 28-AUG-1988
 ; APPLICATION NUMBER: DK 4501/87
 ; FILING DATE: 28-AUG-1987
 ; APPLICATION NUMBER: DK 2254/88
 ; FILING DATE: 26-APR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/466,408
 ; FILING DATE: 21-JUN-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 2361/90
 ; FILING DATE: 25-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/598,337
 ; FILING DATE: 19-NOV-1990
 ; PRIOR APPLICATION DATA:
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 ; FILING DATE: 01-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/598,337
 ; FILING DATE: 01-OCT-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DK91/00299
 ; FILING DATE: 28-AUG-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DK89/00096
 ; FILING DATE: 25-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,687
 ; FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/024,925
 FILING DATE: 26-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Agib, Cheryl H.
 REGISTRATION NUMBER: 34, 086
 REFERENCE/DOCKET NUMBER: 3143-224-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEX/FAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-443-977-59
 ; Query Match 61.7%; Score 203; DB 1; Length 111;
 ; Best Local Similarity 59.6%; Pred. No. 1.1e-17;
 ; Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 Qy 2 PVRCLLPPATGCKARIRWYFVASVSGCQNRFVYGGCRGNNFASSEQMSQCGS 58
 Db 55 PDCFCLSPPTGCKARIRWYFVASVSGCQNRFVYGGCRGNNFASSEQMSQCGS 58

RESULT 13
 US-08-084-718-71
 ; Sequence 71, Application US/08084718
 ; GENERAL INFORMATION:
 ; PATENT NO. 5591603
 ; APPLICANT: Bjorn, Soeren E.
 ; APPLICANT: No. 5591603ris, Kjeld
 ; APPLICANT: Dinesb, Viggo
 ; APPLICANT: No. 5591603bckov-Lauritsen, Leif
 ; APPLICANT: Christensen, Niels D.
 ; APPLICANT: Bregenbaard, Claus
 ; APPLICANT: No. 5591603ris, Fanny
 ; APPLICANT: Petersen, Lars C.
 ; TITLE OF INVENTION: Process for the Preparation of Aprotinin
 ; NUMBER OF SEQUENCES: 83
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: No. 55916030 No. 5591603disk of No. 5591603th America, Inc.
 ; STREET: 405 Lexington Avenue, 62nd Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/084,718
 ; FILING DATE: 19930623
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 4501/87
 ; FILING DATE: 28-AUG-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 2254/88
 ; FILING DATE: 25-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DK88/00138
 ; FILING DATE: 28-AUG-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DK91/00299
 ; FILING DATE: 28-AUG-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DK89/00096
 ; FILING DATE: 25-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,687
 ; FILING DATE: 29-JAN-1992

APPLICANT: Petersen, Lars C.
 TITLE OF INVENTION: Process for the Preparation of Aprotinin
 TITLE OF INVENTION: and Aprotinin Analogs
 NUMBER OF SEQUENCES: 83
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 56210740 NO. 5621074disk of No. 5621074th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,977
 FILING DATE: 18-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/084,718
 FILING DATE: 23-JUN-1993
 APPLICATION NUMBER: DK 4501/87
 FILING DATE: 28-APR-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2254/88
 FILING DATE: 26-APR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK88/00138
 FILING DATE: 28-APR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK89/00096
 FILING DATE: 25-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/466,408
 FILING DATE: 21-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 2361/90
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/598,337
 FILING DATE: 19-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 1118/91
 FILING DATE: 12-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00299
 FILING DATE: 01-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,687
 FILING DATE: 29-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/024,925
 FILING DATE: 26-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Ardis, Cheryl H.
 REGISTRATION NUMBER: 34,086
 REFERENCE/DOCKET NUMBER: 3443.224-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-443-977-71

Query Match Similarity 61.4%; Score 202; DB 1; Length 109;
 Best Local Similarity 61.1%; Pct. No. 1 4e-17; Length 109;
 Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Oy 5 CLIPPATGPKARIIRWYFVAVSGQCNRFVYGGCRGNANNFASBECMMSCOGS 58
 Db 56 CLEPSTGPKARIIRYFVYDATAGLCETFYGGCRANRNFSAEDCMETCGGA 109

Search completed: August 25, 2005, 04:56:24
 Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 25, 2005, 04:45:06 ; Search time 176 Seconds
(without alignments)
163.753 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329
Sequence: 1 YPVRCLLIPATGCKKAR1R.....RGNNNFASEQECMSSCGS 58

Scoring table: BLOSUM62
gapop 10.0 , Gapext 0.5

Searched:

1612378 Seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03;*
1: uniprot_sprot:*,
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	80.2	531	2	Q659F2
2	264	80.2	659	2	Q6ZNM1
3	264	80.2	650	2	Q7Z6B1
4	264	1335	2	Q9I428	homo sapien
5	246	74.8	1280	2	Q8EPX2
6	192	58.4	100	1	BPT1_BOVIN
7	190	57.8	59	2	Q7W311
8	188	57.1	58	2	Q7W412
9	186	56.5	984	2	Q96GN2
10	186	56.5	984	2	Q96GN2
11	185	56.2	327	2	Q6IND9
12	184	55.9	60	1	IBP2_BOVIN
13	177	53.8	100	1	BPT2_BOVIN
14	177	53.8	82	2	Q7Z2T3
15	174	52.9	122	1	UPTR1_PIG
16	172	52.3	80	2	Q8T3S7
17	168	51.1	111	2	Q7M4L3
18	168	51.1	523	2	Q14594
19	168	51.1	738	2	Q9W28
20	168	51.1	738	2	Q6NIZ2
21	168	51.1	751	2	Q60709
22	168	51.1	763	1	APR2_HUMAN
23	168	51.1	763	2	Q7IUT0
24	168	51.1	763	2	Q7IUT0
25	168	51.1	765	1	APR2_RAT
26	166	50.5	283	2	Q6ZNT4
27	166	50.5	576	2	Q8TRB8
28	166	50.5	576	2	Q6UXZ9
29	165	50.2	82	2	Q8WMB4
30	165	50.2	83	2	Q9WAO0
31	50.2	1	SP72_HUMAN		

Scoring table: BLOSUM62
gapop 10.0 , Gapext 0.5

Searched:

1612378 Seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03;*
1: uniprot_sprot:*,
2: uniprot_trembl:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	80.2	531	2	Q659F2
2	264	80.2	659	2	Q6ZNM1
3	264	80.2	650	2	Q7Z6B1
4	264	1335	2	Q9I428	
5	246	74.8	1280	2	Q8EPX2
6	192	58.4	100	1	BPT1_BOVIN
7	190	57.8	59	2	Q7W311
8	188	57.1	58	2	Q7W412
9	186	56.5	984	2	Q96GN2
10	186	56.5	984	2	Q96GN2
11	185	56.2	327	2	Q6IND9
12	184	55.9	60	1	IBP2_BOVIN
13	177	53.8	100	1	BPT2_BOVIN
14	177	53.8	82	2	Q7Z2T3
15	174	52.9	122	1	UPTR1_PIG
16	172	52.3	80	2	Q8T3S7
17	168	51.1	111	2	Q7M4L3
18	168	51.1	523	2	Q14594
19	168	51.1	738	2	Q9W28
20	168	51.1	738	2	Q6NIZ2
21	168	51.1	751	2	Q60709
22	168	51.1	763	1	APR2_HUMAN
23	168	51.1	763	2	Q7IUT0
24	168	51.1	763	2	Q7IUT0
25	168	51.1	765	1	APR2_RAT
26	166	50.5	283	2	Q6ZNT4
27	166	50.5	576	2	Q8TRB8
28	166	50.5	576	2	Q6UXZ9
29	165	50.2	82	2	Q8WMB4
30	165	50.2	83	2	Q9WAO0
31	50.2	1	SP72_HUMAN		

RESULT 1					
ID	0659F2	PRELIMINARY;	PRT;	531 AA.	
AC	0659F2;				
DT	25-OCT-2004 (TREMBLrel. 28, Created)				
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)				
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)				
DR	EMBL: All10280; CAH54061; -.				
KW	Hypothetical protein.				
FT	NON_TER 1				
SQ	SEQUENCE 531 AA; 57158 MW; FEDBBC662369027B CRC64;				
RC	TISSUE=Testis; The German cDNA Consortium; RAB				
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,				
RL	Fobo G., Han M., Wiemann S., Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL: All10280; CAH54061; -.				
KW					
FT	SEQUENCE 531 AA; 57158 MW; FEDBBC662369027B CRC64;				
SQ	Query Match 80.2%; Score 264; DB 2; Length 531; Best Local Similarity 82.8%; Pred. No. 2. 5e-23; Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0; Ov 1 YPVRCLLIPATGCKKAR1R.....RGNNNFASEQECMSSCGS 58				
DB	2 YPVRCLLIPATGCKKAR1R.....RGNNNFASEQECMSSCGS 59				
RN	[1]				
PRELIMINARY;	PRT;	659 AA.			
ID	06ZNM1				
AC	06ZNM1;				
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DR	FLJ00259 protein (Fragment).				
DR	Name=FLJ00259;				
DR	Homo sapiens (Human).				
DR	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; NCBI - TaxID=9606;				
RN	[1]				
SEQUENCE FROM N.A.					
RC	TISSUE=Spleen;				
RA	Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;				
RI	Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.				
CC	-1 SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.				
DR	EMBL; AK131073; BAC85123.1; -.				

DR	GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR	InterPro; IPR03599; Ig-like.
DR	InterPro; IPR01110; Ig-like.
DR	InterPro; IPR03598; Ig_c2.
DR	InterPro; IPR03596; Ig_v.
DR	InterPro; IPR00909; PLAC.
DR	InterPro; IPR02223; Prot_Inh_Kunz-m.
DR	PFam; PF00047; Ig; 1.
DR	PFam; PF00014; Kunz, BPTI; 1.
DR	PRINTS; PR00759; BASICPTSB.
DR	PRINTS; PR00222; Prot_Inh_Kunz-m; 1.
DR	PRODOM; PDD0022; Prot_Inh_Kunz-m; 1.
DR	SMART; SM00409; Ig; 3.
DR	SMART; SM00406; IgV; 3.
DR	SMART; SM00131; KU; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR	PROSITE; PS50835; Ig_LIKE; 3.
DR	PROSITE; PS50900; PLAC; 1.
FT	NON_TER 1
SQ	SEQUENCE 659 AA; 70274 MW; 50FFA993BB44C092 CRC64;
Query Match	80.2%; Score 264; DB 2; Length 659;
Best Local Similarity	82.8%; Pred. No. 3.1e-23;
Matches	48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy	1 YPVRCLLPPATPGCKARIRIWMVAVSGQCNRFVYGGCRQANNAFSEOBMMSSCGS 58
Db	132 YPVRCLLPSAHSGSCDAWAARWVFAVSGQCNRFVYGGCHQANNAFSEOBMMSSCGS 189
RESULT 3	✓
072681	PRELIMINARY; PRT; 660 AA.
072681	PRELIMINARY; PRT; 660 AA.
072681;	AC
072681; 2003	DT
01-OCT-2003 (T-EMBLrel. 25, Last sequence update)	DT
01-MAR-2004 (T-EMBLrel. 26, Last annotation update)	DT
Hypothetical protein.	DE
Db	131 YPVRCLLPSAHSGSCDAWAARWVFAVSGQCNRFVYGGCHQANNAFSEOBMMSSCGS 188
RESULT 4	✓
095428	PRELIMINARY; PRT; 1235 AA.
095428	ID
095428;	AC
01-MAY-1999 (T-EMBLrel. 10, Created)	DT
01-MAY-1999 (T-EMBLrel. 10, Last sequence update)	DT
01-MAR-2004 (T-EMBLrel. 26, Last annotation update)	DT
Hom sapiens (Human).	OS
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelesostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
OX	NCBI_TaxID:9606;
RN	(1)
RP	SEQUENCE FROM N.A.
RA	Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A., Madan A., Dickhoff R., Shaffer T., James R., Labay S., Hood L.; Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC	DR
DR	EMBL; AF09907; AAC97963.1; -.
DR	HSSP; P1211, IKTH.
DR	Genew; HGNC:19262; PAPLN.
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR	InterPro; IPR010294; ADAM_Spacerr1.
DR	InterPro; IPR007110; Ig_Like.
DR	InterPro; IPR003598; Ig_c2.
DR	InterPro; IPR01090; PLAC.
DR	InterPro; IPR002223; Prot_Inh_Kunz-m.
DR	PFam; PF05986; ADAM_Spacerr1; 1.
DR	PFam; PF00047; Ig; 1.
DR	SMART; SM0014; Kunz, BPTI; 1.
DR	PFam; PF00090; TSP1; 5.
DR	PRINTS; PR00759; BASICPTSB.
DR	PRODOM; PDD0022; Prot_Inh_Kunz-m; 1.
DR	SMART; SM00408; IgC2; 3.
DR	SMART; SM00131; KU; 1.
DR	SM00209; TSP1; 5.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR	PROSITE; PS50900; PLAC; 1.
DR	PROSITE; PS50092; TSP1; 5.
DR	Hypothetical protein.
SQ	SEQUENCE 1235 AA; 133476 MW; A0B44CCE4F38E350 CRC64;
Query Match	80.2%; Score 264; DB 2; Length 1235;
Best Local Similarity	82.8%; Pred. No. 5.6e-23;
Matches	48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy	1 YPVRCLLPPATPGCKARIRIWMVAVSGQCNRFVYGGCRQANNAFSEOBMMSSCGS 58
Db	688 YPVRCLLPSAHSGSCDAWAARWVFAVSGQCNRFVYGGCHQANNAFSEOBMMSSCGS 745
RESULT 5	✓
09EPX2	PRELIMINARY; PRT; 1280 AA.
09EPX2	ID
09EPX2;	AC
01-MAR-2001 (T-EMBLrel. 16, Last sequence update)	DT
01-MAR-2001 (T-EMBLrel. 16, Last annotation update)	DT
DT	DE
DE	Papillin.
GN	Name_Papin;
CC	Non-tertiary (Wipros)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TAXID=10090;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RX MEDLINES=20530499; PubMed=11076767;
RA Kramerova T.A., Kawaguchi N., Nelson R.B., Fessler L.I., Chen Y.,
RA Sieron A.L., Prockop D.J., Fessler J.H.;
RT "Papilin in development: a pericellular protein with a homology to the
RT ADAMTS metalloproteinases.";
RL Development 127:5475-5485(2000).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF311171; AAG41980.1; -.
DR HSPB; P12111; 1KTH.
DR MGD; MGI:2386139; Paplin.
DR GO; GO:004167; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001033; Decarboxylase2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR00598; Ig_C2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSPL.
DR Pfam; PF05966; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00890; TSPL; 5.
DR Pfam; PF000759; BASICPTASE.
DR Prodrom; PDD00222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM0131; RU; 1.
DR PROSITE; PS00209; TSPL; 5.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00879; ODR_DC_2_2; UNKNOWN_1.
DR PROSITE; PS00900; PLAC; 1.
DR PROSITE; PS00092; TSPL; 5.
SQ SEQUENCE 1280 AA; 138823 MW; AE287705B5561AF30 CRC64;

Query Match 74.8%; Score 246; DB 2; Length 1280;
Best Local Similarity 75.4%; 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPPVRCILPPATGKARIRWTVAVSGQCRNRTVGGGRGNANNFASQECMSSCG 57
Db 746 YPVRCILPPATGKARIRWTVAVSGQCRNRTVGGGRGNANNFASQECMSSCG 802

RESULT 6

BPTI_BOVIN STANDARD; PRT; 100 AA.

ID BPTI_BOVIN
AC P00974;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pancreatic trypsin inhibitor precursor (Basic protease inhibitor)
DE (BPTI) (Aprotinin).
OS *Bos taurus* (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos;
RN NCBI_TaxID=9913;
RN [1] SEQUENCE FROM N.A.
RP MEDLINES=87833904; PubMed=2441071;
RA Creighton T.B., Charles I.G.;
RT "Sequences of the genes and polypeptide precursors for two bovine
RT protease inhibitors";
RL J. Mol. Biol. 194:11-22(1987).
[2]

RP SEQUENCE FROM N.A.
RK MEDLINES=88285740; PubMed=2456884;
RA Creighton T.E., Charles I.G.;
RT "Biosynthesis, processing, and evolution of bovine pancreatic trypsin
RT inhibitor.";
RT Cold Spring Harb. Symp. Quant. Biol. 52:511-519(1987).
RN [3] SEQUENCE OF 34-97 FROM N.A.
RP MEDLINES=86158754; PubMed=2420326;
RA Kingston I.B., Andron S.;
RT "Sequences encoding two trypsin inhibitors occur in strikingly similar
RT genomic environments";
RT Biochem. J. 233:443-450(1986).
RN [4] SEQUENCE OF 34-97 FROM N.A.
RP MEDLINES=84070725; PubMed=65580617;
RA Anderson S., Kingston I.B.;
RT "Isolation of a genomic clone for bovine pancreatic trypsin inhibitor
RT by using a unique-sequence synthetic DNA probe.";
RT Proc. Natl. Acad. Sci. U.S.A. 80:6838-6842(1983).
RN [5] SEQUENCE OF 36-93, AND DISULFIDE BONDS.
RP MEDLINES=6603012; PubMed=660161;
RA Kasbell B., Laskowski M.;
RT "The basic trypsin inhibitor of bovine pancreas. V. The disulfide
RT linkages.";
RT Biochem. Biophys. Res. Commun. 20:463-468(1965).
RN [6] SEQUENCE OF 36-93, AND DISULFIDE BONDS.
RP MEDLINES=66171231; PubMed=5296424;
RA Anderson F.A., Hornble S.;
RT "The disulfide linkages in kallikrein inactivator of bovine lung.";
J. Biol. Chem. 240:1568-1572(1966).
RN [7] SEQUENCE OF 36-93, AND DISULFIDE BONDS.
RP MEDLINES=68012003; PubMed=605324;
RA Chauvet J., Achet R.;
RT "Covalent structure of a polypeptide inhibitor of trypsin (Kunitz and
Northrop inhibitor).";
RL Bull. Soc. Chim. Biol. 49:985-1000(1967).
RN [8] SEQUENCE OF 36-93.
RP TISSUE_Adrenal chromaffin;
RA Dlouha V., Pospisilova D., Meloun B., Sorm F.;
RT "Sequence of residues 18-20 in pancreatic trypsin inhibitor.";
RT Collect. Czech. Chem. Commun. 33:1363-1365(1968).
RN [9] SEQUENCE OF 36-93.
RP TISSUE_Adrenal chromaffin;
RA Lewis R.V., Ray B., Coguill R., Krugel W.;
RT "Presence of pancreatic trypsin inhibitor in adrenal medullary
RT chromaffin cells";
RT Biochem. Biophys. Res. Commun. 167:543-547(1990).
RN [10] X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RP MEDLINES=9011226; PubMed=2322242;
RA Deisenhofer J., Steigemann W.;
RT "Crystallographic refinement of the structure of bovine pancreatic
RT trypsin inhibitor at 1.5-A resolution.";
RT Acta Crystallogr. B 31:238-250(1975).
RN [11] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP MEDLINES=70255237; PubMed=547861;
RA Huber R., Kukla D., Ruhmann A., Epp O., Formanek H.;
RT "The basic trypsin inhibitor of bovine pancreas. I. Structure analysis
RT and conformation of the polypeptide chain.";
RT Naturwissenschaften 57:389-392(1970).
RN [12] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT GLY-70.
RP MEDLINES=70255237; PubMed=547861;
RA Huber R., Kukla D., Ruhmann A., Epp O., Formanek H.;
RT "The basic trypsin inhibitor of bovine pancreas. I. Structure analysis
RT and conformation of the polypeptide chain.";
RT Naturwissenschaften 57:389-392(1970).
RN [13] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT GLY-70.
RP MEDLINES=9132905; PubMed=714504;
RA Housset D., Kim K.-S., Fuchs J., Woodward C., Wlodawer A.;
RT "Crystal structure of a Y35G mutant of bovine pancreatic trypsin
RT inhibitor.";
RT J. Mol. Biol. 220:757-770(1991).

AC P04815; DR EMBL: M20935; AA51418.1; -; JOINED.
 DT 13-AUG-1987 (Rel. 05; Created)
 DR EMBL; M0931; AA51418.1; JOINED.
 DT 01-MAR-1989 (Rel. 10; Last sequence update)
 DR EMBL; M20933; AA51418.1; JOINED.
 DB Spleen trypsin inhibitor I precursor (SI-I) [Contains: Spleen trypsin inhibitor II (SI-II); Spleen trypsin inhibitor III (SI-III)].
 DE Boa taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Gekkota; Ruminantia; Pecora; Bovidae; Bovine; Bos.
 OC NCBI_TaxID:9913;
 CC RN [1] SPROQUENCE FROM N.A.
 RP MEDLINE=87283904; PubMed=2441071;
 RX Creighton T.B.; Charles T.G.;
 RT "Sequences of the genes and polypeptide precursors for two bovine protease inhibitors.";
 RT J. Mol. Biol. 194:11-22 (1987).
 RN [2] SPROQUENCE FROM N.A.
 RP MEDLINE=88395740; PubMed=2456884;
 RX RA Creighton T.B.; Charles T.G.;
 RT "Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.;"
 RT J. Cold Spring Harb. Symp. Quant. Biol. 52:511-519 (1987).
 RN [3] SPROQUENCE OF 34-97 FROM N.A.
 RP MEDLINE=86158754; PubMed=2420326;
 RX RA Kingstone I.B.; Anderson S.;
 RT "Sequences encoding two trypsin inhibitors occur in strikingly similar genomic environments.;"
 RL Blochem. J. 233:443-450 (1986).
 RN [4] SPROQUENCE OF 34-99.
 RP MEDLINE=89076531; PubMed=2462435;
 RX RA Fioretti E.; Angelletti M.; Fiorucci L.; Barra D.; Bossa F.; Ascoli F.;
 RT "Proteinase-like iso-inhibitors in bovine organs.;"
 RL Biol. Chem. Hoppe-Seyler 369:37-42 (1988).
 RN [5] SPROQUENCE OF 34-99.
 RP TISSUE=Spleen;
 RX MEDLINE=88007630; PubMed=3654647;
 RA Barra D.; Simeone M.; Bossa F.; Fioretti E.; Angelletti M.; Ascoli F.;
 RT "Primary structure of a protease iso-inhibitor from bovine spleen. A possible intermediate in the processing of the primary gene product.;"
 RL J. Biol. Chem. 262:13916-13919 (1987).
 RN [6] SPROQUENCE OF 36-93.
 RP TISSUE=Spleen;
 RX MEDLINE=86008178; PubMed=2413011;
 RA Fioretti E.; Iacopino G.; Angelletti M.; Barra D.; Bossa F.; Ascoli F.;
 RT "Primary structure and anti-proteolytic activity of a Kunitz-type inhibitor from bovine spleen.;"
 RL J. Biol. Chem. 260:11451-11455 (1985).
 RN [7] SPROQUENCE OF 36-97.
 RP TISSUE=Spleen;
 RX MEDLINE=91098258; PubMed=1986787; DOI=10.1016/0167-4838(91)90231-N;
 RA Barra D.; Fioretti E.; Angelletti M.; Marca B.; Bossa F.; Ascoli F.;
 RT "Proteinase iso-inhibitors from bovine spleen: primary structure of an intermediate in the processing of the precursor.;"
 RL Biochim. Biophys. Acta 1076:143-147 (1991).
 CC CC -- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: M20935; AA51418.1; -; JOINED.
 DR EMBL; M0931; AA51418.1; JOINED.
 DR EMBL; M20933; AA51418.1; JOINED.
 DR EMBL; X05275; CA28887.1; -;
 DR EMBL; X06685; CA29881.1; -;
 DR EMBL; X03366; CA27064.1; ALT_SEQ.
 DR EMBL; X03366; CA27065.1; -;
 DR PIR; S00274; TBCSP.
 DR HSSP; P0094; IPR1.
 DR InterPro; IPR00223; Prot_Inh_Kunz-m.
 DR Pfam; PF0014; Kunitz_BPTI; 1.
 DR PRINTS; PRO0759; BASICPTASE.
 DR Direct protein sequencing; Serine Protease inhibitor; Signal.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 33
 FT CHAIN 34 99 Spleen trypsin inhibitor I.
 FT CHAIN 36 97 Spleen trypsin inhibitor III.
 FT CHAIN 36 93 Spleen trypsin inhibitor II.
 FT DOMAIN 40 90 BPTI/Kunitz inhibitor.
 FT SITE 50 51 Reactive bond (By similarity).
 FT DISULFD 40 90 By similarity.
 FT DISULFD 49 73 By similarity.
 FT DISULFD 65 86 By similarity.
 SQ SEQUENCE 100 AA; 10843 MW; 3906973488ACF4E3 CRC64;

Query Match 55.9%; Score 184; DB 1; length 100;
 Best Local Similarity 52.6%; Pred. No. 2.1e-14; Indels 0;
 Matches 30; Conservative 11; Mismatches 16; Indels 0;
 Gap 0;

OY 2 PYRCLLPPATGGKARRIRNWFASYVQCNPFVGGCRGNANNESEQCNSSCGGS 58
 Db 37 PPRCLLPPATGGKARRIRNWFASYVQCNPFVGGCRGNANNESEQCNSSCGGS 93

Query Match 55.9%; Score 184; DB 1; length 100;
 Best Local Similarity 52.6%; Pred. No. 2.1e-14; Indels 0;
 Matches 30; Conservative 11; Mismatches 16; Indels 0;
 Gap 0;

RESULT 14
 07Z2T3 PRELIMINARY; PRT; 82 AA.
 ID 07Z2T3
 AC 07Z2T3
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Amyloid protein b (Fragment).
 GN Name=ppb;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 OC NCBI_TaxID:7955;
 CC RN [1] SPROQUENCE FROM N.A.
 RP RA Groth C.; Lardelli M.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; M0931; AA51418.1; JOINED.
 DR HSSP; Q16019; IARP.
 DR ZFPIN; ZDB-GENE-02020-1; appb.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR00223; Prot_Inh_Kunz-m.
 DR Pfam; PF0014; Kunitz_BPTI; 1.
 DR PRINTS; PRO0759; BASICPTASE.
 DR PRODOM; P000224; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50275; BPTI_KUNITZ_2; 1.
 DR NON_TER 82 82
 FT SEQUENCE 82 AA; 8874 MW; 0723D4AC6585B349 CRC64;

Query Match 53.8%; Score 177; DB 2; length 82;

RESULT 15
UPTI_PIG
TH_PIG
DTC

Search completed: August 25, 2005, 04:55:26
Job time : 180 secs

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: August 25, 2005, 04:49:39 ; Search time 162 Seconds

(without alignments) 140.197 Million cell updates/sec

Title: US-10-721-961-4
perfect score: 329
Sequence: 1 YPVRCLLPPATGPCKARIIR..... RGNANNFASBQECKMSCCGS 58

Scoring table: BLOSUM62 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaai/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaai/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaai/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaai/US07_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/1/pubpaai/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaai/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaai/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaai/US10C_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaai/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaai/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaai/US10_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaai/US10C_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaai/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubpaai/US11C_PUBCOMB.pep:*

21: /cgn2_6/ptodata/1/pubpaai/US60_PUBCOMB.pep:*

22: /cgn2_6/ptodata/1/pubpaai/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

1 329 100.0 58 16 US-10-721-961-4 Sequence 4, Appli

2 326 99.1 58 16 US-10-721-961-5 Sequence 5, Appli

3 314 95.4 58 16 US-10-721-961-7 Sequence 7, Appli

4 314 95.4 111 16 US-10-721-961-34 Sequence 34, Appli

5 291 88.4 58 16 US-10-721-961-6 Sequence 6, Appli

6 291 88.4 111 16 US-10-721-961-33 Sequence 33, Appli

7 264 80.2 58 16 US-10-721-961-1 Sequence 1, Appli

8 264 80.2 111 16 US-10-721-961-32 Sequence 32, Appli

9 264 80.2 15 15 US-10-262-892-92 Sequence 92, Appli

10 264 80.2 1311 14 US-10-103-377C-6 Sequence 6, Appli

11 264 80.2 1311 16 US-10-391-364-91 Sequence 91, Appli

ALIGNMENTS

RESULT 1
US-10-721-961-4

; Sequence 4, Application US/10721961

; Publication No. US20040152633A1

; GENERAL INFORMATION:

; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.

; APPLICANT: Jorgensen, Marianne U

; APPLICANT: Susanne, Bang

; APPLICANT: Olesen, Ole H

; APPLICANT: Petersen, Lars C

; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides

; FILE REFERENCE: 6297-204-US

; CURRENT APPLICATION NUMBER: US/10-721,961

; CURRENT FILING DATE: 2003-11-25

; PRIORITY APPLICATION NUMBER: PCT/DK02/00372

; PRIORITY FILING DATE: 2002-05-31

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 4

; LENGTH: 58

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-721-961-4

; Query Match

; Best Local Similarity 100.0%; Pred. No. 5.6e-32;

; Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 91, Appli

; Sequence 1, Appli

; Sequence 34, Appli

; Sequence 6, Appli

; Sequence 33, Appli

; Sequence 1, Appli

; Sequence 2, Appli

; Sequence 4, Appli

; Sequence 5, Appli

; Sequence 7, Appli

; Sequence 8, Appli

; Sequence 9, Appli

; Sequence 10, Appli

; Sequence 11, Appli

; Sequence 12, Appli

; Sequence 13, Appli

Sequence 86, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 108, Appli
Sequence 173, Appli
Sequence 61, Appli
Sequence 2, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 144, Appli
Sequence 181, Appli
Sequence 55, Appli
Sequence 44, Appli
Sequence 108, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 87, Appli
Sequence 124, Appli
Sequence 173, Appli
Sequence 108, Appli
Sequence 44, Appli
Sequence 1, Appli
Sequence 38, Appli
Sequence 173, Appli
Sequence 44, Appli
Sequence 205, Appli
Sequence 44, Appli
Sequence 29, Appli
Sequence 23, Appli
Sequence 1, Appli

RESULT 2
 US-10-721-961-5
 ; Sequence 5, Application US/10721-961
 ; Publication No. US20040152633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Jorgensen, Marianne U
 ; APPLICANT: Susanne, Bang
 ; APPLICANT: Olesen, Ole H
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: Kunitz-Type sequences and Polypeptides
 ; FILE REFERENCE: 6297_204-US
 ; CURRENT APPLICATION NUMBER: US/10/721, 961
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: US 60/1303, 180
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 5
 ; LENGTH: 58
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-721-961-5

Query Match 99 1%; Score 326; DB 16; Length 58;
 Best Local Similarity 98 3%; Pred. No. 1.3e-31; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 57; Conservative 1; ;

QY 1 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 58
 Db 1 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 58

RESULT 3
 US-10-721-961-7
 ; Sequence 7, Application US/10721-961
 ; GENERAL INFORMATION:
 ; Publication No. US20040152633A1
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Jorgensen, Marianne U
 ; APPLICANT: Susanne, Bang
 ; APPLICANT: Olesen, Ole H
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: Kunitz-Type sequences and Polypeptides
 ; FILE REFERENCE: 6297_204-US
 ; CURRENT APPLICATION NUMBER: US/10/721, 961
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: US 60/1303, 180
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 7
 ; LENGTH: 58
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-721-961-7

Query Match 95 4%; Score 314; DB 16; Length 58;
 Best Local Similarity 94.8%; Pred. No. 3.6e-30; 3; Mismatches 55; Conservative 0; Indels 0; Gaps 0;
 Matches 55; ;

QY 1 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 58
 Db 1 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 58

RESULT 4
 US-10-721-961-34
 ; Sequence 34, Application US/10721-961
 ; Publication No. US20040152633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Jorgensen, Marianne U
 ; APPLICANT: Susanne, Bang
 ; APPLICANT: Olesen, Ole H
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: Kunitz-Type sequences and Polypeptides
 ; FILE REFERENCE: 6297_204-US
 ; CURRENT APPLICATION NUMBER: US/10/721, 961
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: US 60/1303, 180
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 34
 ; LENGTH: 111
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of the 212L-HK118-2 fusion polypeptide
 ; US-10-721-961-34

Query Match 95.4%; Score 314; DB 16; Length 111;
 Best Local Similarity 94.8%; Pred. No. 6.6e-30; 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 55; Conservative 0; ;

QY 1 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 58
 Db 54 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 111

RESULT 5
 US-10-721-961-6
 ; Sequence 6, Application US/10721-961
 ; Publication No. US20040152633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Jorgensen, Marianne U
 ; APPLICANT: Susanne, Bang
 ; APPLICANT: Olesen, Ole H
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: Kunitz-Type sequences and Polypeptides
 ; FILE REFERENCE: 6297_204-US
 ; CURRENT APPLICATION NUMBER: US/10/721, 961
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: US 60/1303, 180
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 6
 ; LENGTH: 58
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-721-961-6

Query Match 88 4%; Score 291; DB 16; Length 58;
 Best Local Similarity 89.7%; Pred. No. 2.1e-27; ;

QY 1 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 58
 Db 1 YPVRCCLPPATGPCKARIRWYFVASVGQCNRFVYGGCRGANNAFSEQCMSSCGS 58

APPLICANT: Rothenberg, Mark,
 APPLICANT: Shmett, Richard,
 APPLICANT: Smithson, Glennida,
 APPLICANT: Spytek, Kimberly,
 APPLICANT: Taupier, Raymond, Jr.,
 APPLICANT: Vernet, Coquine,
 APPLICANT: Voss, Edward,
 APPLICANT: Zerhusen, Brian,
 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 CURRENT APPLICATION NUMBER: US/10/262, 839
 CURRENT FILING DATE: 2002-10-01
 PRIOR APPLICATION NUMBER: 60/326, 483
 PRIOR FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: 60/327, 917
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/328, 029
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/328, 056
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/381, 101
 PRIOR FILING DATE: 2002-05-16
 PRIOR APPLICATION NUMBER: 60/371, 972
 PRIOR FILING DATE: 2002-04-12
 PRIOR APPLICATION NUMBER: 60/327, 342
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 60/328, 044
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/328, 849
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/374, 738
 PRIOR FILING DATE: 2002-04-23
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 367
 SOFTWARE: CirSeqList version 0.1
 SEQ ID NO 92
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-262-839-92

RESULT 10

Query Match 80.2%; Score 264; DB 15; Length 1280;
 Best Local Similarity 82.8%; Pred. No. 6.8e-23; Mismatches 10; Indels 0; Gaps 0;
 Matches 48; Conservative 0; Gaps 0;

Qy 1 YPVRCLLPPATPGCKARIIRWYFVASVQCNRFVYGGCNGNANNFASEBCMSSCGS 58
 Db 732 YPVRCLLPSAHCSCADWAARWFVASVQCNRFWYGGCNGNANNFASEBCMSSCGS 789

RESULT 11

Best Local Similarity 82.8%; Pred. No. 6.8e-23; Mismatches 10; Indels 0; Gaps 0;
 Matches 48; Publication No. US20040121349A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Carroll, Joseph M.
 APPLICANT: Cook, William James
 APPLICANT: Kappeler-Libermann, Rosana
 APPLICANT: Welch, Nadine S.
 APPLICANT: Bandaru, Rajarekhar
 TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352, 55352 AND 65577 MOLECULES AND
 TITLE OF INVENTION: USES THEREFOR
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 09/950, 370
 PRIOR FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: US 60/231, 084
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: US 10/391, 364
 PRIOR FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 60/338, 587
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 10/266, 035
 PRIOR FILING DATE: 2002-10-07
 PRIOR APPLICATION NUMBER: US 10/294, 039
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: US 09/717, 926
 PRIOR FILING DATE: 2000-11-21
 PRIOR APPLICATION NUMBER: US 60/214, 707
 PRIOR FILING DATE: 2000-05-27
 PRIOR APPLICATION NUMBER: US 10/268, 036
 PRIOR FILING DATE: 2002-10-09
 PRIOR APPLICATION NUMBER: US 60/327, 820
 PRIOR FILING DATE: 2001-10-09
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 93
 SOFTWARE: FastSEQ For Windows Version 4.0
 SEQ ID NO 91
 LENGTH: 1311
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-391-364-91

RESULT 12

Query Match 80.2%; Score 264; DB 16; Length 1311;
 Best Local Similarity 82.8%; Pred. No. 6.8e-23; Mismatches 10; Indels 0; Gaps 0;
 Matches 48; Conservative 0; Gaps 0;

Qy 1 YPVRCLLPPATPGCKARIIRWYFVASVQCNRFVYGGCNGNANNFASEBCMSSCGS 58
 Db 732 YPVRCLLPSAHCSCADWAARWFVASVQCNRFWYGGCNGNANNFASEBCMSSCGS 789

RESULT 12

Sequence 86, Application US/10007887
 Publication No. US20030198957A1
 GENERAL INFORMATION:
 APPLICANT: Kekuda, Ramesh
 APPLICANT: Conley, Pamela B.
 APPLICANT: Yang, Ruiy-Bing
 APPLICANT: Hart, Matthew

Query Match 80.2%; Score 264; DB 14; Length 1311;

Query Match 80.2%; Score 264; DB 14; Length 1311;

APPLICANT: Tomlinson, James E.
 APPLICANT: Topper, James N.
 APPLICANT: Shimkets, Richard A.
 APPLICANT: Leach, Martin D.
 APPLICANT: Zerkusen, Bryan D.
 APPLICANT: Komives, Laszlo
 APPLICANT: Padigaru, Muraldhara
 TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 21402-285
 CURRENT APPLICATION NUMBER: US/10/087, 887
 CURRENT FILING DATE: 2002-03-01
 PRIOR APPLICATION NUMBER: 6/0/273, 049
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 6/0/279, 883
 PRIOR FILING DATE: 2001-03-29
 PRIOR APPLICATION NUMBER: 6/0/277, 791
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 6/0/282, 864
 PRIOR FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 6/0/282, 537
 PRIOR FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 6/0/282, 867
 PRIOR FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 104
 SOFTWARE: CuraseqList version 0.1
 SEQ ID NO: 86
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Mus musculus
 ;US-10-087-887-86

Query Match 74.8%; Score 246; DB 14; Length 1280;
 Best Local Similarity 75.4%; Pred. No. 9-8e-21; Mismatches 10; Indels 0; Gaps 0;
 Matches 43; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCLLPAPGCKARTIRWYFYAVSGQCRNFTYGGCRGNANNFASEQCMSSCG 57
 Db 746 YPVRCLLPSAQGSCGDAWRAWYFYVASVGRCNRFWYGGCHGNANNFASEQCMTCRG 802

RESULT 13
 US-08-896-322-5
 Sequence 5, Application US/08896322
 Publication No. US2002010334A1

GENERAL INFORMATION:
 APPLICANT: Werner Schroder, Soren Bjorn, Kjeld No. US2002010334A1, Viggo Dinesen
 TITLE OF INVENTION: APROTININ VARIANTS HAVING IMPROVED PRO
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES: 5
 TITLE OF INVENTION: APROTININ VARIANTS HAVING IMPROVED PRO
 CORRESPONDENCE ADDRESS:
 ADDRESS: SPRUNG KRAMER SCHAEFER & BRISCOE
 STREET: 660 White Plains Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10591-5144

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
 COMPUTER: HP VECTRA
 OPERATING SYSTEM: DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/252, 967
 FILING DATE: 23-Sep-2002
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurt G. Briscoe
 REGISTRATION NUMBER: 33, 141
 REFERENCE/DOCKET NUMBER: Bayer 9911-KGB

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 332-1700
 TELEFAX: (914) 332-1844
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 57 Amino acids
 TYPE: Amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: Linear
 ORIGINAL SOURCE:
 ORGANISM: Aprotinin variant

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ;US-10-252-967-5

Query Match 58.7%; Score 193; DB 14; Length 57;
 Best Local Similarity 57.4%; Pred. No. 1 2e-15;
 Matches 31; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 5 CLPPATCPKARIIRWYFASVGQCRFVYGGCRGNANNFASEQECMSCCGS 58
 Db 4 CLEPPSTGPCRAIRYFYDATAGLCETFVYGGCRANRNNFSAEDCMTCCGA 57

RESULT 15
 US-09-234-874A-7
 ; Sequence 7, Application US/09234874A
 Publication No. US20010020003A1

GENERAL INFORMATION:

APPLICANT: White, Tyler R.
 Damm, Deborah
 McFadden, Kathleen
 Garrick, Brett L.
 Lesikar, David D.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES

NUMBER OF SEQUENCES: 228

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0. Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/234,874A
 FILING DATE: 11-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/436,555
 FILING DATE: 08-MAY-1995

ATTORNEY/AGENT INFORMATION:

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INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 ; US-09-234-874A-7

Query Match 58.4%; Score 192; DB 9; Length 58;
 Best Local Similarity 57.9%; Pred. No. 1 7e-15;
 Matches 33; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

Qy 2 PYRCLLPPATCPKARIIRWYFASVGQCRFVYGGCRGNANNFASEQECMSCCGS 58
 Db 2 PPFCLLEPPATCPKARIIRWYFASVGQCRFVYGGCRGNANNFASEQECMSCCGS 58

Search completed: August 25, 2005, 04:59:08
 Job time : 164 secs

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